

Alpha Virus nspl alignment

CLUSTAL W (1.82) multiple sequence alignment

SFV_nsp1	MAAK--VHVDIEADSPFIKSLQKAFPSFEVESLQVTPNDHANARAFSHLATKLIEQETDK --MK--VTVDEADSPFLKALQKAFPAFEVESQVTPNDHANARAFSHLATKLIEQEVPA -MDS--VYVDIDADSAFLKALQQAYPMFEVEPKQVTPNDHANARAFSHLAIKLIQEIDP -MEK--VHVDIEEDSPFLRALQRSFPQFEVEAKQVTNDHANARAFSHLASKLIETEVDP -MEKPVVNVDVDPQSPFVVQLQKSFQFEVVAQQVT PNDHANARAFSHLASKLIELEVPT	58 56 57 57 59
SFV_nsp1	DTIILDIGSAPSRRMMSTHKYHCVCPMRS AEDPERLDSYAKKLAASGKVLDREIAGKIT NITILDVGSA PARRLMSDH SYH CICPMKSAEDPERLANYARKLAKTAGEVLDKNVSGKIT DSTIILDIGSAPARRMMMSDRK YHCVCPMRS AEDPERLANYARKLASAAGKVTDKNISGKIN SDT IILDIGSAPARRMYSKH KYH CICPMRCAEDPDRLYKYATKLKNCKEITDKELDKKMK TATIILDIGSAPARRMFSEHQYHCVCPMRS P EDPDRMMKYASKLAEKACKITKNKLHEKIK	118 116 117 117 119
SFV_nsp1	DLQTVMATPDAESPTFCLHTDVTCRTAAEVAVYQDVYAVHAPTSLYHQAMGVRTAYWIG DLQDVMATPDLESPTFCLHTDETCRTRAEVAVYQD--VHAPTSLYHQAMGVRTVY WIG DLQAVMAVPNMETSTFCLHTDATCKQRGDVAIYQDVYAVHAPTSLYHQAIKGVRVAYWIG ELAAVMSDPDLETE MCLH DDESCRYEGQVAVYQDVYAVDGPTSLYHQANKGVRVAYWIG DLRTVLDTPDAETPSLCFHNDVTCNMRAEYSVMDVY-INAPGTIYHQAMGVRTLYWIG	178 173 177 177 178
SFV_nsp1	DLQTVMATPDAESPTFCLHTDVTCRTAAEVAVYQDVYAVHAPTSLYHQAMGVRTAYWIG DLQDVMATPDLESPTFCLHTDETCRTRAEVAVYQD--VHAPTSLYHQAMGVRTVY WIG DLQAVMAVPNMETSTFCLHTDATCKQRGDVAIYQDVYAVHAPTSLYHQAIKGVRVAYWIG ELAAVMSDPDLETE MCLH DDESCRYEGQVAVYQDVYAVDGPTSLYHQANKGVRVAYWIG DLRTVLDTPDAETPSLCFHNDVTCNMRAEYSVMDVY-INAPGTIYHQAMGVRTLYWIG	178 173 177 177 178
SFV_nsp1	FDTTPFMFDALAGAYPTYATNWADEQVLQARNIGLCAASLTEGRLGKLSILRKKQLKPCD FDTTPFMFVVAGAYPTYSTNWADEQVLQARNIGLCATSLSEHRGKISIMRKKRLR PSD FDTTPFMYNAMEGAYPSYSTNWADEQVLKAKNIGLCSTDLS EGRRGKLSIMRGKKL KPCD FDTTPFMFKNLAGAYPSYSTNWADETVLTARNIGLCSSDVMERSRRGMSILRKKYLKPSN FDTTQFMSAMAGSYPAYNTNWADEKVLEARNIGLCSTKLSEGRTGKLSIMRKKELKPGS	238 233 237 237 238
SFV_nsp1	TVMFSVGSTLYTESRKLLRSWHLPSVFHLKGKQSFTCRCDTIVSCEGYVVKKITMCPGLY -RMESVG-TLYIESRRLLKSWHLPSVFHLKGKNSFTCRCDTIVSCEGYVVKKITMSPGTY RVLFSVGSTLYPESRKLLQSWHLPSVFHLKGKLSFTCRCDTIVSCEGYVVKKRVTMSPGIY NVLFSVGSTIYHEKDLLRSWHLPSVFHLRGKQNYTCRCETIVSCDGYVVKKRIAISPGLY RVYFSVGSTLYPEHRASLQSWHLPSVFHLNGKQSYTCRCDTVVSCEGYVVKKITISPGIT	298 291 297 297 298
SFV_nsp1	GKTVGYAVTYHAEGFLVCKTTDTVKGERSFPVCTYVPSTICDQMTGILATDVT PEDAQK GKTVGYAVTHAEGFLMCKVTDVRGERVSFPVCTYVPATICDQMTGILATDVT PEDAQK GKTSGYAVTHHAGGFLMCKTTDTVGERVSFSVCTYVPATICDQMTGILATEVTPEDAQK GKPSGYAATMHREGFLCCVTDLNGERVSFPVCTYVPATLCDQMTGILATDVSADDAQK GETVGYAVTHNSEGFLCKVTDVKGERSFPVCTYIPATICDQMTGIMATDISPDDAQK	358 351 357 357 358
SFV_nsp1	LLVGLNQRI VVNGRTQRNTNTMKNYLLPIAVAVAFSKWAREYKADLDDEKPLGVRERSLTC LLVGLNQRI VVNGRTQRNTNTMKNYLLPVVAQAFSKWAREAKADMEDEKPLGTRERTLTC LLVGLNQRI VVNGRTQRNTNTMKNYLLPIVAQAFSKWAKECRKDMED EKLLGV RERTLTC LLVGLNQRI VVNGRTQRNTNTMKNYLLPVVAQAFARWAKEKEYKEDQEDERPLGLRDRQLVM LLVGLNQRI VINGRTNRNTNTMQNYLLPIIAQGFSK WAKERKDDLDNEKMLGTRERKLTY	418 411 417 417 418
SFV_nsp1	CCLWAFKTRKMHTMYKPDQTIVKVPSEFNSFVIPSLWSTGLAI PVR SRIKMLLA KKT CCLWAFKNHKHTHMYKRPDTQTIVKVPSTFD S FVIPSLWSSSLSIGIRQRIKLLLGPKLS CCLWAFRKHKHTVYKRPDTQSIQKVPAEFDSFVIPSLWSSGLSIPLRTRIKWLLSKAPK GCCWAFRRHKITSIYKRPDTQTIIKVNSDFHSFVLP RIGSNTLEIGL RTRIRKML EEEHKE GCLWAFRTKKVHSFYRPPGTQTCVKVPASFSAFPMSSWTTSLPMSLRQLKLALQPKKE	478 471 477 477 478
SFV_nsp1	-RELI PVLD-ASSARDAE QEEKERLEAE LTREALPPLVPIAPAETG-VVDVDVEELEYHA -RDL PYSGD-RNEAREAEKEAEETKEAE LTREALPPLVGSNCADD--VDQVDVEEELTYRA YEQLPHSGN-AEEAAQAE TDAVEE QEAELTREAMPPLQ--ATQDDI-QVEIDV E QLEDRA PSPLITAED-IQEAKCAADEAKEVREAEELRAALPPLA--ADFEEP-TLEADVDI MLQEA EKLLQVSEELVMEAKAAFEDAQEEARAEKLREALPPLVADKGIEAAAEEVCEVEGLQADI	535 527 533 533 538

SFV_nsp1	GA 537
RRV_nsp1	GA 529
ONV_nsp1	GA 535
VEEV_nsp1	GA 535
SinV_nsp1	GA 540
	**